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RAW SEQUENCE LISTING

DATE: 05/13/2002

PATENT APPLICATION: US/10/008,566

TIME: 09:35:31

Input Set : A:\DX01341 seq listing.ST25.txt

Output Set: N:\CRF3\05102002\J008566.raw

3 <110> APPLICANT: Reche-Gallardo, Pedro A.
 4 Soumelis, Vassili
 5 Liu, Yong-Jun
 6 de Waal Malefyt, Rene
 7 Bazan, Jose F.
 8 Kastelein, Robert A.

10 <120> TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
 12 <130> FILE REFERENCE: dx01341
 14 <140> CURRENT APPLICATION NUMBER: 10/008566
 C--> 15 <141> CURRENT FILING DATE: 2002-04-30
 17 <150> PRIOR APPLICATION NUMBER: US 60/298268
 18 <151> PRIOR FILING DATE: 2001-06-14
 20 <150> PRIOR APPLICATION NUMBER: US 60/247218
 21 <151> PRIOR FILING DATE: 2000-11-10
 23 <160> NUMBER OF SEQ ID NOS: 6
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1658
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (23)..(1399)
 35 <223> OTHER INFORMATION:
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39	ctctctctct atctctctca ga atg aca att cta ggt aca act ttt ggc atg	52
40	Met Thr Ile Leu Gly Thr Thr Phe Gly Met	
41	1 5 10	
43	gtt ttt tct tta ctt caa gtc gtt tct gga gaa agt ggc tat gct caa	100
44	Val Phe Ser Leu Leu Gln Val Val Ser Gly Glu Ser Gly Tyr Ala Gln	
45	15 20 25	
47	aat gga gac ttg gaa gat gca gaa ctg gat gac tac tca ttc tca tgc	148
48	Asn Gly Asp Leu Glu Asp Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys	
49	30 35 40	
51	tat agc cag ttg gaa gtg aat gga tgc cag cat tca ctg acc tgt gct	196
52	Tyr Ser Gln Leu Glu Val Asn Gly Ser Gln His Ser Leu Thr Cys Ala	
53	45 50 55	
55	ttt gag gac cca gat gtc aac acc acc aat ctg gaa ttt gaa ata tgt	244
56	Phe Glu Asp Pro Asp Val Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys	
57	60 65 70	
59	ggg gcc ctc gtg gag gta aag tgc ctg aat ttc agg aaa cta caa gag	292
60	Gly Ala Leu Val Glu Val Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu	
61	75 80 85 90	

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63 ata tat ttc atc gag aca aag aaa ttc tta ctg att gga aag agc aat      340
64 Ile Tyr Phe Ile Glu Thr Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn
65          95          100          105
67 ata tgt gtg aag gtt gga gaa aag agt cta acc tgc aaa aaa ata gac      388
68 Ile Cys Val Lys Val Gly Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp
69          110          115          120
71 cta acc act ata gtt aaa cct gag gct cct ttt gac ctg agt gtc atc      436
72 Leu Thr Thr Ile Val Lys Pro Glu Ala Pro Phe Asp Leu Ser Val Ile
73          125          130          135
75 tat cgg gaa gga gcc aat gac ttt gtg gtg aca ttt aat aca tca cac      484
76 Tyr Arg Glu Gly Ala Asn Asp Phe Val Val Thr Phe Asn Thr Ser His
77          140          145          150
79 ttg caa aag aag tat gta aaa gtt tta atg cat gat gta gct tac cgc      532
80 Leu Gln Lys Lys Tyr Val Lys Val Leu Met His Asp Val Ala Tyr Arg
81 155          160          165          170
83 cag gaa aag gat gaa aac aaa tgg acg cat gtg aat tta tcc agc aca      580
84 Gln Glu Lys Asp Glu Asn Lys Trp Thr His Val Asn Leu Ser Ser Thr
85          175          180          185
87 aag ctg aca ctc ctg cag aga aag ctc caa ccg gca gca atg tat gag      628
88 Lys Leu Thr Leu Leu Gln Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu
89          190          195          200
91 att aaa gtt cga tcc atc cct gat cac tat ttt aaa ggc ttc tgg agt      676
92 Ile Lys Val Arg Ser Ile Pro Asp His Tyr Phe Lys Gly Phe Trp Ser
93          205          210          215
95 gaa tgg agt cca agt tat tac ttc aga act cca gag atc aat aat agc      724
96 Glu Trp Ser Pro Ser Tyr Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser
97          220          225          230
99 tca ggg gag atg gat cct atc tta cta acc atc agc att ttg agt ttt      772
100 Ser Gly Glu Met Asp Pro Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe
101 235          240          245          250
103 ttc tct gtc gct ctg ttg gtc atc ttg gcc tgt gtg tta tgg aaa aaa      820
104 Phe Ser Val Ala Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys
105          255          260          265
107 agg att aag cct atc gta tgg ccc agt ctc ccc gat cat aag aag act      868
108 Arg Ile Lys Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr
109          270          275          280
111 ctg gaa cat ctt tgt aag aaa cca aga aaa aat tta aat gtg agt ttc      916
112 Leu Glu His Leu Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe
113          285          290          295
115 aat cct gaa agt ttc ctg gac tgc cag att cat agg gtg gat gac att      964
116 Asn Pro Glu Ser Phe Leu Asp Cys Gln Ile His Arg Val Asp Asp Ile
117          300          305          310
119 caa gct aga gat gaa gtg gaa ggt ttt ctg caa gat acg ttt cct cag      1012
120 Gln Ala Arg Asp Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln
121 315          320          325          330
123 caa cta gaa gaa tct gag aag cag agg ctt gga ggg gat gtg cag agc      1060
124 Gln Leu Glu Glu Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser
125          335          340          345
127 ccc aac tgc cca tct gag gat gta gtc gtc act cca gaa agc ttt gga      1108

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128 Pro Asn Cys Pro Ser Glu Asp Val Val Val Thr Pro Glu Ser Phe Gly
129          350          355          360
131 aga gat tca tcc ctc aca tgc ctg gct ggg aat gtc agt gca tgt gac 1156
132 Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys Asp
133          365          370          375
135 gcc cct att ctc tcc tct tcc agg tcc cta gac tgc agg gag agt ggc 1204
136 Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly
137          380          385          390
139 aag aat ggg cct cat gtg tac cag gac ctc ctg ctt agc ctt ggg act 1252
140 Lys Asn Gly Pro His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr
141 395          400          405          410
143 aca aac agc acg ctg ccc cct cca ttt tct ctc caa tct gga atc ctg 1300
144 Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu
145          415          420          425
147 aca ttg aac cca gtt gct cag ggt cag ccc att ctt act tcc ctg gga 1348
148 Thr Leu Asn Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly
149          430          435          440
151 tca aat caa gaa gaa gca tat gtc acc atg tcc agc ttc tac caa aac 1396
152 Ser Asn Gln Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn
153          445          450          455
155 cag tgaagtgtaa gaaaccacaga ctgaacttac cgtgagcgac aaagatgatt 1449
156 Gln
159 taaaaggga gtctagagtt cctagtctcc ctacacagcac agagaagaca aaattagcaa 1509
161 aaccccaacta cacagtctgc aagattctga aacattgctt tgaccactct tctgagttc 1569
163 agtggcactc aacatgagtc aagagcatcc tgcttctacc atgtggattt ggtcacaagg 1629
165 tttaagtgta cccaatgatt cagctattt 1658
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169 <211> LENGTH: 459
170 <212> TYPE: PRT
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173 <400> SEQUENCE: 2
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176 1          5          10          15
179 Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp
180          20          25          30
183 Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
184          35          40          45
187 Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
188          50          55          60
191 Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
192 65          70          75          80
195 Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
196          85          90          95
199 Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
200          100          105          110
203 Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
204          115          120          125
207 Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn
208          130          135          140

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211 Asp Phe Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val
212 145 150 155 160
215 Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
216 165 170 175
219 Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
220 180 185 190
223 Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
224 195 200 205
227 Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
228 210 215 220
231 Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro
232 225 230 235 240
235 Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu
236 245 250 255
239 Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val
240 260 265 270
243 Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys
244 275 280 285
247 Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu
248 290 295 300
251 Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val
252 305 310 315 320
255 Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu
256 325 330 335
259 Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu
260 340 345 350
263 Asp Val Val Val Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser Leu Thr
264 355 360 365
267 Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser
268 370 375 380
271 Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val
272 385 390 395 400
275 Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro
276 405 410 415
279 Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala
280 420 425 430
283 Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala
284 435 440 445
287 Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
288 450 455
291 <210> SEQ ID NO: 3
292 <211> LENGTH: 1557
293 <212> TYPE: DNA
294 <213> ORGANISM: Homo sapiens
296 <220> FEATURE:
297 <221> NAME/KEY: CDS
298 <222> LOCATION: (13)..(1125)
299 <223> OTHER INFORMATION:
302 <400> SEQUENCE: 3

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303 cggcacgagg gc atg ggg cgg ctg gtt ctg ctg tgg gga gct gcc gtc ttt      51
304           Met Gly Arg Leu Val Leu Leu Trp Gly Ala Ala Val Phe
305           1           5           10
307 ctg ctg gga ggc tgg atg gct ttg ggg caa gga gga gca gca gaa gga      99
308 Leu Leu Gly Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly
309           15           20           25
311 gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca      147
312 Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr
313 30           35           40           45
315 tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga      195
316 Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg
317           50           55           60
319 ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag      243
320 Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln
321           65           70           75
323 gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac      291
324 Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp
325           80           85           90
327 att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca      339
328 Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala
329           95           100           105
331 agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg      387
332 Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val
333 110           115           120           125
335 aga ttt tcg tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg      435
336 Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu
337           130           135           140
339 tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac      483
340 Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp
341           145           150           155
343 acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa      531
344 Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu
345           160           165           170
347 ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct      579
348 Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala
349           175           180           185
351 atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag      627
352 Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu
353 190           195           200           205
355 gtg aca tgc tgg cag aga ggc gag att cgg gat gcc tgt gca gag aca      675
356 Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr
357           210           215           220
359 cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc      723
360 Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser
361           225           230           235
363 ctg gcc atc ctt ctg atg gtg tct ctc ctc ctt ctg tct tta tgg aaa      771
364 Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys
365           240           245           250
367 tta tgg aga gtg aag aag ttt ctc att ccc agc gtg cca gac ccg aaa      819

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